

4/3



SUBSTITUTE SEQUENCE LISTING

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Jarvis, Eric
Sangamo BioSciences, Inc.

<120> Regulation of Angiogenesis With Zinc
Finger Proteins

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<150> US 09/733,604

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1          5

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    <400> 131
Arg Ser Asp His Leu Ala Arg
1          5

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    <400> 132
Arg Ser Asp Asn Leu Ala Arg
1          5

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<210> 133
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 1 5

<210> 134
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<220>
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<400> 134
 Asp Arg Ser Asn Leu Thr Arg
 1 5

<210> 135
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<220>
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<400> 135
 Arg Ser Asp Ala Leu Thr Arg
 1 5

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<220>
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<400> 136
 Gln Ser Gly His Leu Gln Arg
 1 5

<210> 137
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<220>
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<400> 137
 Arg Ser Asp Ala Leu Thr Gln
 1 5

<210> 138

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gaagaggacc 10

    <210> 139
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    <220>
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    <400> 139
gggggcgctc 10

    <210> 140
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    <210> 141
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ggggcggggg 10

    <210> 142
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ggggaggatc 10

    <210> 143
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gggggtgacc	10
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<211> 7	

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 1                               5

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    <220>
    <223> finger

    <400> 150
Arg Ser Asp Asn Leu Thr Arg
 1                               5

    <210> 151
    <211> 7
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    <220>
    <223> finger

    <400> 151
Gln Arg Ser Asn Leu Val Arg
 1                               5

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    <212> PRT
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    <220>
    <223> finger

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Gln Ser Ser Asp Leu Arg Arg
 1                               5

    <210> 153
    <211> 7
    <212> PRT
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    <220>
    <223> finger

    <400> 153
Gln Ser Ser His Leu Ala Arg
 1                               5

    <210> 154
    <211> 7
    <212> PRT

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    <213> Artificial Sequence

    <220>
    <223> finger

    <400> 154
Arg Ser Asp His Leu Ser Arg
1           5

    <210> 155
    <211> 7
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> finger

    <400> 155
Gln Ser Ser His Leu Ala Arg
1           5

    <210> 156
    <211> 7
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> finger

    <400> 156
Arg Ser Asp His Leu Thr Thr
1           5

    <210> 157
    <211> 7
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> finger

    <400> 157
Arg Ser Asp Ala Leu Ala Arg
1           5

    <210> 158
    <211> 7
    <212> PRT
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    <220>
    <223> finger

    <400> 158
Lys Thr Ser His Leu Arg Ala
1           5

    <210> 159
    <211> 7
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    <220>
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Arg Ser Asp Glu Leu Gln Arg
 1                      5

    <210> 160
    <211> 7
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    <220>
    <223> finger

    <400> 160
Arg Ser Asp His Leu Ser Lys
 1                      5

    <210> 161
    <211> 7
    <212> PRT
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    <220>
    <223> finger

    <400> 161
Thr Thr Ser Asn Leu Arg Arg
 1                      5

    <210> 162
    <211> 7
    <212> PRT
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    <220>
    <223> finger

    <400> 162
Arg Ser Ser Asn Leu Gln Arg
 1                      5

    <210> 163
    <211> 7
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    <220>
    <223> finger

    <400> 163
Arg Ser Asp His Leu Ser Arg
 1                      5

    <210> 164
    <211> 7
    <212> PRT
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    <220>
    <223> finger

    <400> 164
Asp Arg Ser His Leu Thr Arg
 1                5

    <210> 165
    <211> 7
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> finger

    <400> 165
Arg Ser Asp His Leu Thr Arg
 1                5

    <210> 166
    <211> 7
    <212> PRT
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    <220>
    <223> finger

    <400> 166
Gln Ser Ser Asp Leu Thr Arg
 1                5

    <210> 167
    <211> 7
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> finger

    <400> 167
Asp Arg Ser Asn Leu Thr Arg
 1                5

    <210> 168
    <211> 7
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> finger

    <400> 168
Thr Ser Gly His Leu Val Arg
 1                5

    <210> 169
    <211> 7
    <212> PRT
    <213> Artificial Sequence

    <220>

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    <223> finger

    <400> 169
Arg Ser Asp His Leu Ser Arg
1          5

    <210> 170
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    <220>
    <223> finger

    <400> 170
Asp Arg Ser Asn Leu Thr Arg
1          5

    <210> 171
    <211> 7
    <212> PRT
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    <220>
    <223> finger

    <400> 171
Met Ser His His Leu Ser Arg
1          5

    <210> 172
    <211> 7
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> finger

    <400> 172
Arg Ser Asp His Leu Ser Arg
1          5

    <210> 173
    <211> 7
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    <220>
    <223> finger

    <400> 173
Arg Ser Asp Asn Leu Ala Arg
1          5

    <210> 174
    <211> 7
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> finger

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<400> 174
Arg Ser Asp His Leu Ser Arg
1 5

<210> 175
<211> 7
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<220>
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<400> 175
Arg Ser Asp Asn Leu Thr Gln
1 5

<210> 176
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<220>
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Asp Arg Ser Ser Leu Thr Arg
1 5

<210> 177
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<220>
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Arg Ser Asp His Leu Ser Arg
1 5

<210> 178
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Gln Ser Gly Ser Leu Thr Arg
1 5

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Gln Ser Gly Ser Leu Thr Arg
1 5

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<220>
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Gln Ser Gly His Leu Gln Arg
1 5

<210> 181
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<220>
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<400> 181
Gln Ser Ser Asp Leu Thr Arg
1 5

<210> 182
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<220>
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<400> 182
ggagaggggg cgcagtg

18

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<220>
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<400> 183
atggacgggt gaggcggcg

19

<210> 184
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<220>
<223> target

<400> 184
gggggtgac

9

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 <400> 185
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9

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 <400> 186
 Arg Ser Asp Ala Leu Thr Arg
 1 5

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 <220>
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 <400> 187
 Gln Ser Gly Asp Leu Thr Arg
 1 5

<210> 188
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 <400> 188
 Glu Arg Gly Asp Leu Thr Arg
 1 5

<210> 189
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 <220>
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 <400> 189
 Arg Ser Asp His Leu Ala Arg
 1 5

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 <220>
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 <400> 190
 Arg Ser Asp Asn Leu Ala Arg
 1 5

<210> 191
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<220>
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<400> 191
 Gln Ser Ser His Leu Ala Arg
 1 5

<210> 192
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<220>
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<400> 192
 Arg Ser Asp Glu Leu Thr Arg
 1 5

<210> 193
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<220>
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<400> 193
 Arg Ser Asp Glu Leu Gln Arg
 1 5

<210> 194
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<220>
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<400> 194
 Arg Ser Asp Asn Leu Ala Arg
 1 5

<210> 195
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    <400> 195
Arg Ser Asp His Leu Ala Arg
1           5

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    <220>
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    <400> 196
Asp Arg Ser Asn Leu Thr Arg
1           5

    <210> 197
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    <220>
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    <400> 197
Arg Ser Asp Ala Leu Thr Gln
1           5

    <210> 198
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    <223> recognition helix

    <400> 198
Asp Arg Ser Asn Leu Thr Arg
1           5

    <210> 199
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    <220>
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    <400> 199
Met Ser His His Leu Ser Arg
1           5

    <210> 200
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    <220>
    <223> recognition helix

    <400> 200
Arg Ser Asp His Leu Ser Arg
1           5

    <210> 201
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    <400> 201
Asp Arg Ser His Leu Thr Arg
1           5

    <210> 202
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    <212> PRT
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    <220>
    <223> recognition helix

    <400> 202
Arg Ser Asp His Leu Thr Arg
1           5

    <210> 203
    <211> 7
    <212> PRT
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    <220>
    <223> recognition helix

    <400> 203
Gln Ser Ser Asp Leu Thr Arg
1           5

    <210> 204
    <211> 20
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> VEGF-C forward primer

    <400> 204
tgccgatgca tgtctaaact

    <210> 205
    <211> 22
    <212> DNA
    <213> Artificial Sequence

    <220>

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20

<223> VEGF-C reverse primer

<400> 205
tgaacagggtc tcttcatcca gc 22

<210> 206
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> VEGF-C probe

<221> modified_base
<222> (1)...(1)
<223> n = c modified by aminofluorescein (FAM)

<221> modified_base
<222> (26)...(26)
<223> n = a modified by tetramethylrhodamine (TAMRA)

<400> 206
nagcaacact accacagtgt caggcn 26

<210> 207
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> target

<400> 207
tgagcggcgg cagcggagc 19

<210> 208
<211> 25
<212> PRT
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<220>
<223> exemplary DNA-binding subdomain motif of C-2H-2
class of zinc finger proteins (ZFP)

<221> MOD_RES
<222> (2)...(5)
<223> Xaa = any amino acid, Xaa in positions 4 and 5 may
be present or absent

<221> MOD_RES
<222> (7)...(18)
<223> Xaa = any amino acid

<221> MOD_RES
<222> (20)...(24)
<223> Xaa = any amino acid, Xaa in positions 23 and 24
may be present or absent

<400> 208
Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His
20 25

<210> 209
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> target

<400> 209
ggcgtagac

9

<210> 210
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> target

<400> 210
ggcgacgta

9

<210> 211
<211> 5
<212> PRT
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<220>
<223> peptide linker

<400> 211
Thr Gly Glu Lys Pro
1 5

<210> 212
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide linker

<400> 212
Gly Gly Gly Gly Ser
1 5

<210> 213
<211> 8
<212> PRT
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<220>
<223> peptide linker

<400> 213
Gly Gly Arg Arg Gly Gly Gly Ser
1 5

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<210> 214
<211> 9
<212> PRT
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<220>
<223> peptide linker

<400> 214
Leu Arg Gln Arg Asp Gly Glu Arg Pro
1          5

<210> 215
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide linker

<400> 215
Leu Arg Gln Lys Asp Gly Gly Gly Ser Glu Arg Pro
1          5          10

<210> 216
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide linker

<400> 216
Leu Arg Gln Lys Asp Gly Gly Gly Ser Gly Gly Gly Ser Glu Arg Pro
1          5          10          15

<210> 217
<211> 30
<212> PRT
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<220>
<223> F1 DNA binding domain of mouse transcription
      factor Zif268

<400> 217
Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp
1          5          10          15
Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro
      20          25          30

<210> 218
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> F2 DNA binding domain of mouse transcription
      factor Zif268

<400> 218

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Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu
 1 5 10 15
 Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro
 20 25

<210> 219
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> F3 DNA binding domain of mouse transcription
 factor Zif268

<400> 219
 Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg
 1 5 10 15
 Lys Arg His Thr Lys Ile His Leu Arg Gln Lys
 20 25

<210> 220
 <211> 9
 <212> DNA
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<220>
 <223> mouse transcription factor Zif268 target

<400> 220
 gcgtgggcg

9

<210> 221
 <211> 94
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Sp-1 transcription factor

<400> 221
 Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly Cys Gly Lys
 1 5 10 15
 Val Tyr Gly Lys Thr Ser His Leu Arg Ala His Leu Arg Trp His Thr
 20 25 30
 Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg Phe
 35 40 45
 Thr Arg Ser Asp Glu Leu Gln Arg His Lys Arg Thr His Thr Gly Glu
 50 55 60
 Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met Arg Ser Asp
 65 70 75 80
 His Leu Ser Lys His Ile Lys Thr His Gln Asn Lys Lys Gly
 85 90

<210> 222
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 <212> DNA
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<220>
 <223> Sp-1 optimal target consensus sequence

<400> 222
ggggcgggg

<210> 223
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Sp-i consensus sequence with leader sequence

<400> 223
Met Glu Lys Leu Arg Asn Gly Ser Gly Asp Pro Gly Lys Lys Lys Gln
1 5 10 15
His Ala Cys Pro Glu Cys Gly Lys Ser Phe Ser Lys Ser Ser His Leu
20 25 30
Arg Ala His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Lys Cys Pro
35 40 45
Glu Cys Gly Lys Ser Phe Ser Arg Ser Asp Glu Leu Gln Arg His Gln
50 55 60
Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Pro Glu Cys Gly Lys
65 70 75 80
Ser Phe Ser Arg Ser Asp His Leu Ser Lys His Gln Arg Thr His Gln
85 90 95
Asn Lys Lys Gly
100

<210> 224
<211> 7
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<220>
<223> N-terminal nuclear localization signal from SV40
large T antigen

<400> 224
Pro Lys Lys Lys Arg Lys Val
1 5

<210> 225
<211> 8
<212> PRT
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<220>
<223> FLAG peptide

<400> 225
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 226
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> VEGF-A forward primer

<400> 226

gtgcattgga gccttgcctt g 21

<210> 227
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VEGF-A reverse primer

<400> 227
 actcgatctc atcagggtac tc 22

<210> 228
 <211> 25
 <212> DNA
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<220>
 <223> VEGF-A Taqman probe

<221> modified_base
 <222> (1)...(1)
 <223> n = c modified by aminofluorescein (FAM)

<221> modified_base
 <222> (25)...(25)
 <223> n = a modified by tetramethylrhodamine (TAMRA)

<400> 228
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<210> 229
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GAPDH forward primer

<400> 229
 ccatgttcgt catgggtgtg a 21

<210> 230
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GAPDH reverse primer

<400> 230
 catggactgt ggtcatgagt 20

<210> 231
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GAPDH Taqman probe

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<221> modified_base
<222> (1)...(1)
<223> n = t modified by aminofluorescein (FAM)

<221> modified_base
<222> (24)...(24)
<223> n = a modified by tetramethylrhodamine (TAMRA)

<400> 231
ncctgcacca ccaactgctt agcn                                     24

<210> 232
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> VP16-FLAG forward primer

<400> 232
catgacgatt tcgatctgga                                         20

<210> 233
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> VP16-FLAG reverse primer

<400> 233
ctacttgatca tcgtcgctct tg                                     22

<210> 234
<211> 26
<212> DNA
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<220>
<223> VP16-FLAG Taqman probe

<221> modified_base
<222> (1)...(1)
<223> n = a modified by aminofluorescein (FAM)

<221> modified_base
<222> (26)...(26)
<223> n = a modified by tetramethylrhodamine (TAMRA)

<400> 234
ntcggtaaac atctgctcaa actcgn                                     26

<210> 235
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> RT-PCR primer

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<400> 235
 atgaactttc tgctgtcttg ggtgcatt 28

 <210> 236
 <211> 22
 <212> DNA
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 <220>
 <223> RT-PCR primer

 <400> 236
 tcaccgcctc ggcttgtcac at 22

 <210> 237
 <211> 18
 <212> DNA
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 <220>
 <223> murine VEGF target

 <400> 237
 tgagcggcgg cagcggag 18

 <210> 238
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> recognition helix

 <400> 238
 Arg Ser Asp Glu Leu Ser Arg
 1 5

 <210> 239
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> recognition helix

 <400> 239
 Gln Ser Gly His Leu Thr Lys
 1 5

 <210> 240
 <211> 10
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> target

 <400> 240
 gctgggggcg 10


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<210> 241
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 241
cccagatctg gtgatggcaa gaagaagcag caccatctgc cacatccag
49

<210> 242
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 242
cccaagctta ggatccaccc ttcttgttct ggtgggt
37

<210> 243
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> VZ+57

<400> 243
His Gln Asn Lys Lys Gly Gly Ser Gly Asp Gly Lys Lys Lys Gln His
1      5      10      15
Ile Cys

<210> 244
<211> 9
<212> DNA
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